FIGURE 1

```
   1   GAACCAGCCT GCACGCGCTG GCTCCGGGTG ACAGCCGCGC GCCTCGGCCA

  51   GGATCTGAGT GATGAGACGT GTCCCCACTG AGGTGCCCCA CAGCAGCAGG

 101   TGTTGAGCAT GGGCTGAGAA GCTGGACCGG CACCAAAGGG CTGGCAGAAA

 151   TGGGCGCCTG GCTGATTCCT AGGCAGTTGG CGGCAGCAAG GAGGAGAGGC

 201   CGCAGCTTCT GGAGCAGAGC CGAGACGAAG CAGTTCTGGA GTGCCTGAAC

 251   GGCCCCCTGA GCCCTACCCG CCTGGCCCAC TATGGTCCAG AGGCTGTGGG

 301   TGAGCCGCCT GCTGCGGCAC CGGAAAGCCC AGCTCTTGCT GGTCAACCTG

 351   CTAACCTTTG GCCTGGAGGT GTGTTTGGCC GCAGGCATCA CCTATGTGCC

 401   GCCTCTGCTG CTGGAAGTGG GGGTAGAGGA GAAGTTCATG ACCATGGTGC

 451   TGGGCATTGG TCCAGTGCTG GGCCTGGTCT GTGTCCCGCT CCTAGGCTCA

 501   GCCAGTGACC ACTGGCGTGG ACGCTATGGC CGCCGCCGGC CCTTCATCTG

 551   GGCACTGTCC TTGGGCATCC TGCTGAGCCT CTTTCTCATC CCAAGGGCCG

 601   GCTGGCTAGC AGGGCTGCTG TGCCCGGATC CCAGGCCCCT GGAGCTGGCA

 651   CTGCTCATCC TGGGCGTGGG GCTGCTGGAC TTCTGTGGCC AGGTGTGCTT

 701   CACTCCACTG GAGGCCCTGC TCTCTGACCT CTTCCGGGAC CCGGACCACT

 751   GTCGCCAGGC CTACTCTGTC TATGCCTTCA TGATCAGTCT TGGGGGCTGC

 801   CTGGGCTACC TCCTGCCTGC CATTGACTGG GACACCAGTG CCCTGGCCCC

 851   CTACCTGGGC ACCCAGGAGG AGTGCCTCTT TGGCCTGCTC ACCCTCATCT

 901   TCCTCACCTG CGTAGCAGCC ACACTGCTGG TGGCTGAGGA GGCAGCGCTG

 951   GGCCCCACCG AGCCAGCAGA AGGGCTGTCG GCCCCCTCCT TGTCGCCCCA

1001   CTGCTGTCCA TGCCGGGCCC GCTTGGCTTT CCGGAACCTG GGCGCCCTGC

1051   TTCCCCGGCT GCACCAGCTG TGCTGCCGCA TGCCCCGCAC CCTGCGCCGG

1101   CTCTTCGTGG CTGAGCTGTG CAGCTGGATG GCACTCATGA CCTTCACGCT

1151   GTTTTACACG GATTTCGTGG GCGAGGGGCT GTACCAGGGC GTGCCCAGAG

1201   CTGAGCCGGG CACCGAGGCC CGGAGACACT ATGATGAAGG CGTTCGGATG

1251   GGCAGCCTGG GGCTGTTCCT GCAGTGCGCC ATCTCCCTGG TCTTCTCTCT

1301   GGTCATGGAC CGGCTGGTGC AGCGATTCGG CACTCGAGCA GTCTATTTGG

1351   CCAGTGTGGC AGCTTTCCCT GTGGCTGCCG GTGCCACATG CCTGTCCCAC

1401   AGTGTGGCCG TGGTGACAGC TTCAGCCGCC CTCACCGGGT TCACCTTCTC
```

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FIGURE 1 – continued

```
1451   AGCCCTGCAG ATCCTGCCCT ACACACTGGC CTCCCTCTAC CACCGGGAGA

1501   AGCAGGTGTT CCTGCCCAAA TACCGAGGGG ACACTGGAGG TGCTAGCAGT

1551   GAGGACAGCC TGATGACCAG CTTCCTGCCA GGCCCTAAGC CTGGAGCTCC

1601   CTTCCCTAAT GGACACGTGG GTGCTGGAGG CAGTGGCCTG CTCCCACCTC

1651   CACCCGCGCT CTGCGGGGCC TCTGCCTGTG ATGTCTCCGT ACGTGTGGTG

1701   GTGGGTGAGC CCACCGAGGC CAGGGTGGTT CCGGGCCGGG GCATCTGCCT

1751   GGACCTCGCC ATCCTGGATA GTGCCTTCCT GCTGTCCCAG GTGGCCCCAT

1801   CCCTGTTTAT GGGCTCCATT GTCCAGCTCA GCCAGTCTGT CACTGCCTAT

1851   ATGGTGTCTG CCGCAGGCCT GGGTCTGGTC GCCATTTACT TTGCTACACA

1901   GGTAGTATTT GACAAGAGCG ACTTGGCCAA ATACTCAGCG TAGAAAACTT

1951   CCAGCACATT GGGGTGGAGG GCCTGCCTCA CTGGGTCCCA GCTCCCCGCT

2001   CCTGTTAGCC CCATGGGGCT GCCGGGCTGG CCGCCAGTTT CTGTTGCTGC

2051   CAAAGTAATG TGGCTCTCTG CTGCCACCCT GTGCTGCTGA GGTGCGTAGC

2101   TGCACAGCTG GGGGCTGGGG CGTCCCTCTC CTCTCTCCCC AGTCTCTAGG

2151   GCTGCCTGAC TGGAGGCCTT CCAAGGGGGT TTCAGTCTGG ACTTATACAG

2201   GGAGGCCAGA AGGGCTCCAT GCACTGGAAT GCGGGGACTC TGCAGGTGGA

2251   TTACCCAGGC TCAGGGTTAA CAGCTAGCCT CCTAGTTGAG ACACACCTAG

2301   AGAAGGGTTT TTGGGAGCTG AATAAACTCA GTCACCTGGT TTCCCATCTC

2351   TAAGCCCCTT AACCTGCAGC TTCGTTTAAT GTAGCTCTTG CATGGGAGTT

2401   TCTAGGATGA AACACTCCTC CATGGGATTT GAACATATGA AAGTTATTTG

2451   TAGGGGAAGA GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC

2501   CACAGCACTG TCTTTTTGCT GATCCACCCC CCTCTTACCT TTTATCAGGA

2551   TGTGGCCTGT TGGTCCTTCT GTTGCCATCA CAGAGACACA GGCATTTAAA

2601   TATTTAACTT ATTTATTTAA CAAAGTAGAA GGGAATCCAT TGCTAGCTTT

2651   TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA

2701   GGTCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT

2751   CTCCTGGGGT CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC

2801   TACTCATCCC AAATGATAAT TCCAAATGCT GTTACCCAAG GTTAGGGTGT
```

FIGURE 1 - continued

```
2851   TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT CTCAACGGCT TCCCTAACCA

2901   CCCCTCTTCT CTTGGCCCAG CCTGGTTCCC CCCACTTCCA CTCCCCTCTA

2951   CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAAT TTCCCCTACC

3001   CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT

3051   TGGAGCTACT GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTTG

3101   TCCATCTCAG CCCCCAGAGT ATATCTGTGC TTGGGGAATC TCACACAGAA

3151   ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG GAGGTCTTAT CTCTCAGGGG

3201   GGGGTTTAAG TGCCGTTTGC AATAATGTCG TCTTATTTAT TTAGCGGGGT

3251   GAATATTTTA TACTGTAAGT GAGCAATCAG AGTATAATGT TTATGGTGAC

3301   AAAATTAAAG GCTTTCTTAT
```

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FIGURE 2

```
  1   MVQRLWVSRL LRHRKAQLLL VNLLTFGLEV CLAAGITYVP PLLLEVGVEE
 51   KFMTMVLGIG PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL
101   FLIPRAGWLA GLLCPDPRPL ELALLILGVG LLDFCGQVCF TPLEALLSDL
151   FRDPDHCRQA YSVYAFMISL GGCLGYLLPA IDWDTSALAP YLGTQEECLF
201   GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH CCPCRARLAF
251   RNLGALLPRL HQLCCRMPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL
301   YQGVPRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG
351   TRAVYLASVA AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA
401   SLYHREKQVF LPKYRGDTGG ASSEDSLMTS FLPGPKPGAP FPNGHVGAGG
451   SGLLPPPPAL CGASACDVSV RVVVGEPTEA RVVPGRGICL DLAILDSAFL
501   LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ VVFDKSDLAK
551   YSA
```

FIGURE 3

```
DcSUT2    1 MENGTKELNKPQPPSSAAMQLQTPVQKIPTATWKLVLVAAIAAGVQFGWA 50
             .|      .   .:        .|.||   :   |.:     |
PROST03   1 ................MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLA 33

         51 LQLSLLTPYVQLLGIPHKWAAYIWLCGPISGMLVQPIVGYYSDHCQSSFG 100
             :..  |  . .|:  |.   :    ||: |:. |:.|  |||  . :|
         34 AGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASDHWRGRYG 83

        101 RRRPFIASGAGCVAISVILIGFAADISYKAGDDMSKTLKPRAVTVFVIGF 150
             ||||| . . : :|. || |  |:        | :| . . :|
         84 RRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDP....RPLELALLILGV 129

        151 WILDVANNMLQGPCRALLADLCSGDTRRMRSANAFYSFFMAVGNILGYAA 200
             :||       .   |||.|| |       |   |.| ...| |||
        130 GLLDFCGQVCFTPLEALLSDLFR.DPDHCRQAYSVYAFMISLGGCLGYLL 178

        201 GSYN.NLYKLFPFSKTHACDLYCANLKSCFIISIALLIIITVVALSVVRE 249
             . . .  | |: |    |:        | | |::     ||
        179 PAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEP 228

        250 NSGPPDDADAAEEPPSSGKIPV..FGELLGALKDL....PRPMLLLLIVT 293
             |     . .      |     ::    | ||   |      || :   |  :
        229 AEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAE 278

        294 CLNWIAWFPFILFDTDWMGREIYGGT......AGQGKLYDQGVRAGALGL 337
             .|.|   ||| ||||..|   :| |          :  ||:||| |.||| 
        279 LCSWMALMTFTLFYTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGL 328

        338 LLNSVVLGLTSIAVEYLVRGVGGVKILWGFVNFILAIGLVMTVVVSKVAQ 387
             |    :  .   |:  .:  ||.  |      . |   . |          ||
        329 FLQCAISLVFSLVMDRLVQRFGTRAV...........YLASVAAFPVAA 366

        388 HQREHSANGQLLPPSAGVKAGALSLFSILGIPLSITYSIPFALASIYSSG 437
             | . .     ||.       | ||  |. | |  |
        367 GATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRG 416

        438 SGAGQGLSLGVLNLAIVVPQMIVSVLAGPFDSLFGGGNLPAFVVGAISAA 487
             |       .:   :   |.   |         . | | . ||
        417 DTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASAC 466

        488 ISGVLAIVLLPKPSKDAASKLSLSGTYH.................... 515
             |  :|   |    .:     :
        467 DVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQL 516
```

FIGURE 4

```
       GAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGAGT
    1  --------+---------+---------+---------+---------+---------+ 60
       CTTGGTCGGACGTGCGCGACCGAGGCCCACTGTCGGCGCGCGGAGCCGGTCCTAGACTCA

       GATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAA
   61  --------+---------+---------+---------+---------+---------+ 120
       CTACTCTGCACAGGGGTGACTCCACGGGGTGTCGTCGTCCACAACTCGTACCCGACTCTT

       GCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGG
  121  --------+---------+---------+---------+---------+---------+ 180
       CGACCTGGCCGTGGTTTCCCGACCGTCTTTACCCGCGGACCGACTAAGGATCCGTCAACC

       CGGCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGA
  181  --------+---------+---------+---------+---------+---------+ 240
       GCCGTCGTTCCTCCTCTCCGGCGTCGAAGACCTCGTCTCGGCTCTGCTTCGTCAAGACCT

       GTGCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGG
  241  --------+---------+---------+---------+---------+---------+ 300
       CACGGACTTGCCGGGGGACTCGGGATGGGCGGACCGGGTGATACCAGGTCTCCGACACCC

   c                                                    M  V  Q  R  L  W  V -

       TGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG
  301  --------+---------+---------+---------+---------+---------+ 360
       ACTCGGCGGACGACGCCGTGGCCTTTCGGGTCGAGAACGACCAGTTGGACGATTGGAAAC

   c     S  R  L  L  R  H  R  K  A  Q  L  L  L  V  N  L  L  T  F  G -

       GCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGG
  361  --------+---------+---------+---------+---------+---------+ 420
       CGGACCTCCACACAAACCGGCGTCCGTAGTGGATACACGGCGGAGACGACGACCTTCACC

   c     L  E  V  C  L  A  A  G  I  T  Y  V  P  P  L  L  L  E  V  G -

       GGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCT
  421  --------+---------+---------+---------+---------+---------+ 480
       CCCATCTCCTCTTCAAGTACTGGTACCACGACCCGTAACCAGGTCACGACCCGGACCAGA

   c     V  E  E  K  F  M  T  M  V  L  G  I  G  P  V  L  G  L  V  C -

       GTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGC
  481  --------+---------+---------+---------+---------+---------+ 540
       CACAGGGCGAGGATCCGAGTCGGTCACTGGTGACCGCACCTGCGATACCGGCGGCGGCCG

   c     V  P  L  L  G  S  A  S  D  H  W  R  G  R  Y  G  R  R  R  P -

       CCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCG
  541  --------+---------+---------+---------+---------+---------+ 600
       GGAAGTAGACCCGTGACAGGAACCCGTAGGACGACTCGGAGAAAGAGTAGGGTTCCCGGC

   c     F  I  W  A  L  S  L  G  I  L  L  S  L  F  L  I  P  R  A  G -

       GCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCC
  601  --------+---------+---------+---------+---------+---------+ 660
       CGACCGATCGTCCCGACGACACGGGCCTAGGGTCCGGGGACCTCGACCGTGACGAGTAGG

   c     W  L  A  G  L  L  C  P  D  P  R  P  L  E  L  A  L  L  I  L -

       TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC
  661  --------+---------+---------+---------+---------+---------+ 720
       ACCCGCACCCCGACGACCTGAAGACACCGGTCCACACGAAGTGAGGTGACCTCCGGGACG

   c     G  V  G  L  L  D  F  C  G  Q  V  C  F  T  P  L  E  A  L  L -
```

FIGURE 4 – continued

```
        TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCA
    721 ---------+---------+---------+---------+---------+---------+ 780
        AGAGACTGGAGAAGGCCCTGGGCCTGGTGACAGCGGTCCGGATGAGACAGATACGGAAGT

    C       S   D   L   F   R   D   P   D   H   C   R   Q   A   Y   S   V   Y   A   F   M  -

        TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTG
    781 ---------+---------+---------+---------+---------+---------+ 840
        ACTAGTCAGAACCCCCGACGGACCCGATGGAGGACGGACGGTAACTGACCCTGTGGTCAC

    C       I   S   L   G   G   C   L   G   Y   L   L   P   A   I   D   W   D   T   S   A  -

        CCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCT
    841 ---------+---------+---------+---------+---------+---------+ 900
        GGGACCGGGGGATGGACCCGTGGGTCCTCCTCACGGAGAAACCGGACGAGTGGGAGTAGA

    C       L   A   P   Y   L   G   T   Q   E   E   C   L   F   G   L   L   T   L   I   F  -

        TCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCG
    901 ---------+---------+---------+---------+---------+---------+ 960
        AGGAGTGGACGCATCGTCGGTGTGACGACCACCGACTCCTCCGTCGCGACCCGGGGTGGC

    C       L   T   C   V   A   A   T   L   L   V   A   E   E   A   A   L   G   P   T   E  -

        AGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCC
    961 ---------+---------+---------+---------+---------+---------+ 1020
        TCGGTCGTCTTCCCGACAGCCGGGGGAGGAACAGCGGGGTGACGACAGGTACGGCCCGGG

    C       P   A   E   G   L   S   A   P   S   L   S   P   H   C   C   P   C   R   A   R  -

         GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCA
    1021 ---------+---------+---------+---------+---------+---------+ 1080
         CGAACCGAAAGGCCTTGGACCCGCGGGACGAAGGGGCCGACGTGGTCGACACGACGGCGT

    C       L   A   F   R   N   L   G   A   L   L   P   R   L   H   Q   L   C   C   R   M  -

         TGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGA
    1081 ---------+---------+---------+---------+---------+---------+ 1140
         ACGGGGCGTGGGACGCGGCCGAGAAGCACCGACTCGACACGTCGACCTACCGTGAGTACT

    C       P   R   T   L   R   R   L   F   V   A   E   L   C   S   W   M   A   L   M   T  -

         CCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAG
    1141 ---------+---------+---------+---------+---------+---------+ 1200
         GGAAGTGCGACAAAATGTGCCTAAAGCACCCGCTCCCCGACATGGTCCCGCACGGGTCTC

    C       F   T   L   F   Y   T   D   F   V   G   E   G   L   Y   Q   G   V   P   R   A  -

         CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGG
    1201 ---------+---------+---------+---------+---------+---------+ 1260
         GACTCGGCCCGTGGCTCCGGGCCTCTGTGATACTACTTCCGCAAGCCTACCCGTCGGACC

    C       E   P   G   T   E   A   R   R   H   Y   D   E   G   V   R   M   G   S   L   G  -

         GGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC
    1261 ---------+---------+---------+---------+---------+---------+ 1320
         CCGACAAGGACGTCACGCGGTAGAGGGACCAGAAGAGAGACCAGTACCTGGCCGACCACG

    C       L   F   L   Q   C   A   I   S   L   V   F   S   L   V   M   D   R   L   V   Q  -

         AGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCG
    1321 ---------+---------+---------+---------+---------+---------+ 1380
         TCGCTAAGCCGTGAGCTCGTCAGATAAACCGGTCACACCGTCGAAAGGGACACCGACGGC

    C       R   F   G   T   R   A   V   Y   L   A   S   V   A   A   F   P   V   A   A   G  -
```

FIGURE 4 - continued

```
        GTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGT
   1381 ---------+---------+---------+---------+---------+---------+ 1440
        CACGGTGTACGGACAGGGTGTCACACCGGCACCACTGTCGAAGTCGGCGGGAGTGGCCCA

  c      A   T   C   L   S   H   S   V   A   V   V   T   A   S   A   A   L   T   G   F -

        TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGA
   1441 ---------+---------+---------+---------+---------+---------+ 1500
        AGTGGAAGAGTCGGGACGTCTAGGACGGGATGTGTGACCGGAGGGAGATGGTGGCCCTCT

  c      T   F   S   A   L   Q   I   L   P   Y   T   L   A   S   L   Y   H   R   E   K -

        AGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC
   1501 ---------+---------+---------+---------+---------+---------+ 1560
        TCGTCCACAAGGACGGGTTTATGGCTCCCCTGTGACCTCCACGATCGTCACTCCTGTCGG

  c      Q   V   F   L   P   K   Y   R   G   D   T   G   G   A   S   S   E   D   S   L -

        TGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGG
   1561 ---------+---------+---------+---------+---------+---------+ 1620
        ACTACTGGTCGAAGGACGGTCCGGGATTCGGACCTCGAGGGAAGGGATTACCTGTGCACC

  c      M   T   S   F   L   P   G   P   K   P   G   A   P   F   P   N   G   H   V   G -

        GTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTG
   1621 ---------+---------+---------+---------+---------+---------+ 1680
        CACGACCTCCGTCACCGGACGAGGGTGGAGGTGGGCGCGAGACGCCCCGGAGACGGACAC

  c      A   G   G   S   G   L   L   P   P   P   P   A   L   C   G   A   S   A   C   D -

        ATGTCTCCGTACGTGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGG
   1681 ---------+---------+---------+---------+---------+---------+ 1740
        TACAGAGGCATGCACACCACCACCCACTCGGGTGGCTCCGGTCCCACCAAGGCCCGGCCC

  c      V   S   V   R   V   V   V   G   E   P   T   E   A   R   V   V   P   G   R   G -

        GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCAT
   1741 ---------+---------+---------+---------+---------+---------+ 1800
        CGTAGACGGACCTGGAGCGGTAGGACCTATCACGGAAGGACGACAGGGTCCACCGGGGTA

  c      I   C   L   D   L   A   I   L   D   S   A   F   L   L   S   Q   V   A   P   S -

        CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTG
   1801 ---------+---------+---------+---------+---------+---------+ 1860
        GGGACAAATACCCGAGGTAACAGGTCGAGTCGGTCAGACAGTGACGGATATACCACAGAC

  c      L   F   M   G   S   I   V   Q   L   S   Q   S   V   T   A   Y   M   V   S   A -

        CCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCG
   1861 ---------+---------+---------+---------+---------+---------+ 1920
        GGCGTCCGGACCCAGACCAGCGGTAAATGAAACGATGTGTCCATCATAAACTGTTCTCGC

  c      A   G   L   G   L   V   A   I   Y   F   A   T   Q   V   V   F   D   K   S   D -

        ACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCTCA
   1921 ---------+---------+---------+---------+---------+---------+ 1980
        TGAACCGGTTTATGAGTCGCATCTTTTGAAGGTCGTGTAACCCCACCTCCCGGACGGAGT

  c      L   A   K   Y   S   A   * -

        CTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTT
   1981 ---------+---------+---------+---------+---------+---------+ 2040
        GACCCAGGGTCGAGGGGCGAGGACAATCGGGGTACCCCGACGGCCCGACCGGCGGTCAAA
```

FIGURE 4 - continued

```
      CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGC
2041  ---------+---------+---------+---------+---------+---------+ 2100
      GACAACGACGGTTTCATTACACCGAGAGACGACGGTGGGACACGACGACTCCACGCATCG

      TGCACAGCTGGGGGGCTGGGGCGTCCCTCTCCTCTCTCCCCAGTCTCTAGGGCTGCCTGAC
2101  ---------+---------+---------+---------+---------+---------+ 2160
      ACGTGTCGACCCCCGACCCCGCAGGGAGAGGAGAGAGGGGTCAGAGATCCCGACGGACTG

      TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT
2161  ---------+---------+---------+---------+---------+---------+ 2220
      ACCTCCGGAAGGTTCCCCCAAAGTCAGACCTGAATATGTCCCTCCGGTCTTCCCGAGGTA

      GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT
2221  ---------+---------+---------+---------+---------+---------+ 2280
      CGTGACCTTACGCCCCTGAGACGTCCACCTAATGGGTCCGAGTCCCAATTGTCGATCGGA

      CCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGT
2281  ---------+---------+---------+---------+---------+---------+ 2340
      GGATCAACTCTGTGTGGATCTCTTCCCAAAAACCCTCGACTTATTTGAGTCAGTGGACCA

      TTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTT
2341  ---------+---------+---------+---------+---------+---------+ 2400
      AAGGGTAGAGATTCGGGGAATTGGACGTCGAAGCAAATTACATCGAGAACGTACCCTCAA

      TCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGA
2401  ---------+---------+---------+---------+---------+---------+ 2460
      AGATCCTACTTTGTGAGGAGGTACCCTAAACTTGTATACTTTCAATAAACATCCCCTTCT

      GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
2461  ---------+---------+---------+---------+---------+---------+ 2520
      CAGGACTCCCCGTTGTGTGTTCTTGGTCCAGGGGAGTCGGGTGTCGTGACAGAAAAACGA

      GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
2521  ---------+---------+---------+---------+---------+---------+ 2580
      CTAGGTGGGGGGGAGAATGGAAAATAGTCCTACACCGGACAACCAGGAAGACAACGGTAGT

      CAGAGACACAGGCATTTAAATATTTAACTTATTTATTTAACAAAGTAGAAGGGAATCCAT
2581  ---------+---------+---------+---------+---------+---------+ 2640
      GTCTCTGTGTCCGTAAATTTATAAATTGAATAAATAAATTGTTTCATCTTCCCTTAGGTA

      TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA
2641  ---------+---------+---------+---------+---------+---------+ 2700
      ACGATCGAAAAGACACAACCACAGATTATAAACCCATCCCACCCCCTAGGGGTTGTTAGT

      GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGT
2701  ---------+---------+---------+---------+---------+---------+ 2760
      CCAGGGGACTCTATCGACCAGTAACCCGACTAGTAACGGTCTTAGAAGAAGAGGACCCCA

      CTGGCCCCCCAAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT
2761  ---------+---------+---------+---------+---------+---------+ 2820
      GACCGGGGGGTTTTACGGATTGGGTCCTGGAACCTTTAAGATGAGTAGGGTTTACTATTA

      TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCTTCAGGT
2821  ---------+---------+---------+---------+---------+---------+ 2880
      AGGTTTACGACAATGGGTTCCAATCCCACAACTTCCTTCCATCTCCCACCCCGAAGTCCA

      CTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA
2881  ---------+---------+---------+---------+---------+---------+ 2940
      GAGTTGCCGAAGGGATTGGTGGGGAGAAGAGAACCGGGTCGGACCAAGGGGGGTGAAGGT

      CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC
2941  ---------+---------+---------+---------+---------+---------+ 3000
      GAGGGGAGATGAGAGAGATCCTGACCCGACTACTTCCGTGACGGGTTTTAAAGGGGATGG
```

FIGURE 4 - continued

```
      CCCAACTTTCCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
3001  ---------+---------+---------+---------+---------+---------+  3060
      GGGTTGAAAGGGGATGGGGGTTGAAAGGGGTGGTCGAGGTGTTGGGACAAACCTCGATGA


      GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
3061  ---------+---------+---------+---------+---------+---------+  3120
      CGTCCTGGTCTTCGTGTTTCACGCCAAAGGGTTCGGAAACAGGTAGAGTCGGGGGTCTCA


      ATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCCTGCCTGAGCTAAGG
3121  ---------+---------+---------+---------+---------+---------+  3180
      TATAGACACGAACCCCTTAGAGTGTGTCTTTGAGTCCTCGTGGGGGACGGACTCGATTCC


      GAGGTCTTATCTCTCAGGGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
3181  ---------+---------+---------+---------+---------+---------+  3240
      CTCCAGAATAGAGAGTCCCCCCCCCAAATTCACGGCAAACGTTATTACAGCAGAATAAATA


      TTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC
3241  ---------+---------+---------+---------+---------+---------+  3300
      AATCGCCCCACTTATAAAATATGACATTCACTCGTTAGTCTCATATTACAAATACCACTG


      AAAATTAAAGGCTTTCTTAT
3301  ---------+---------+  3320
      TTTTAATTTCCGAAAGAATA
```

Figure 5
Expression of Prost 3 in Human Tissue

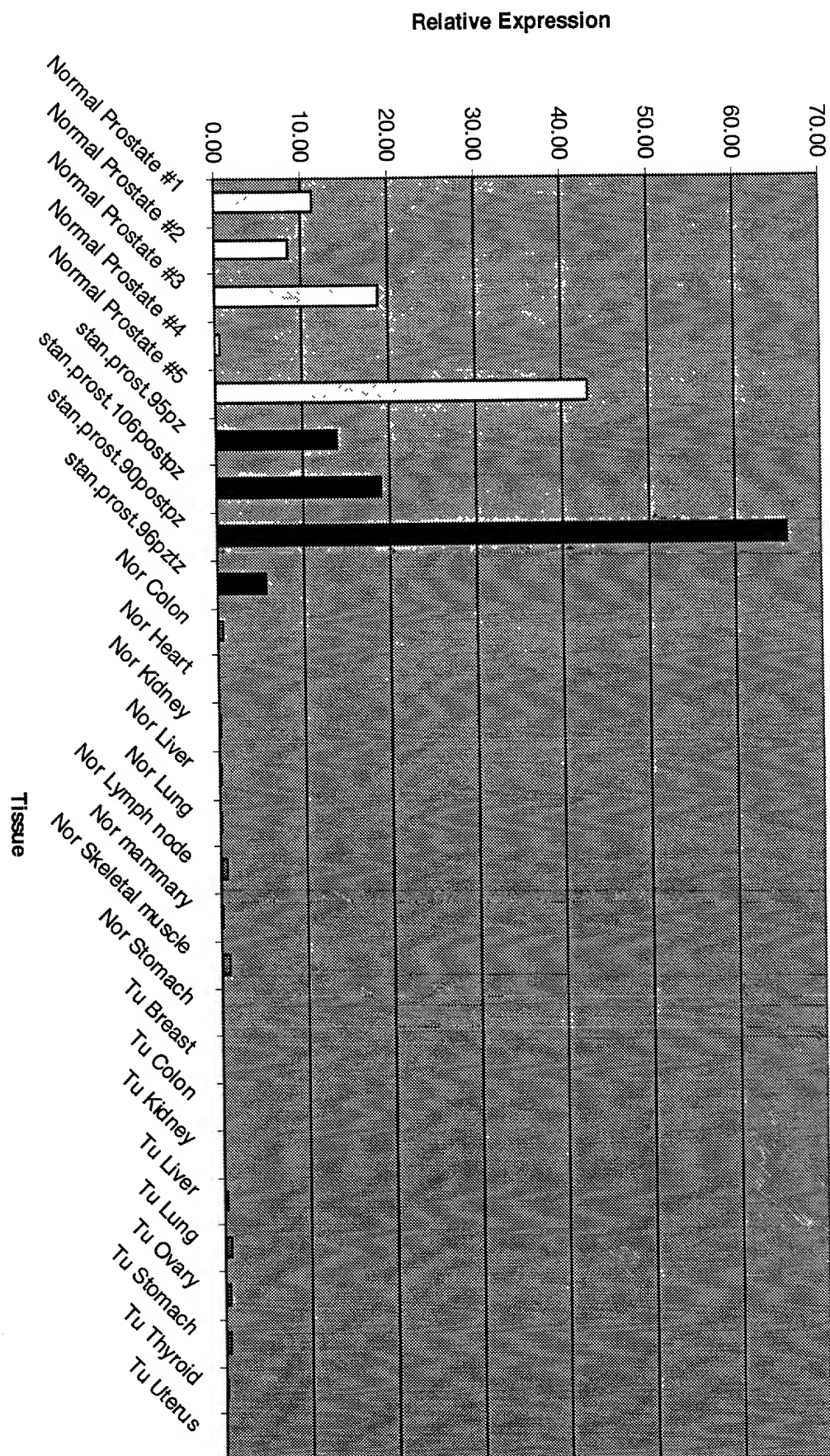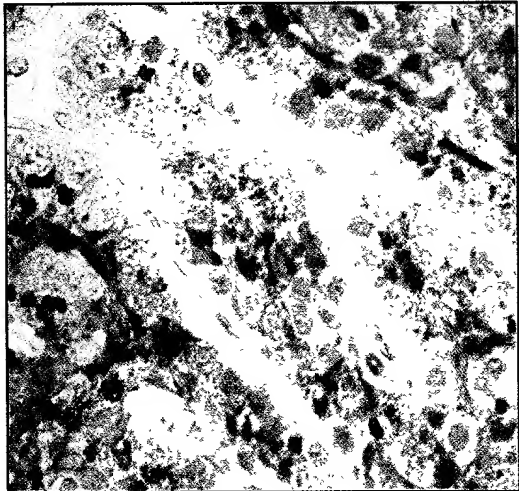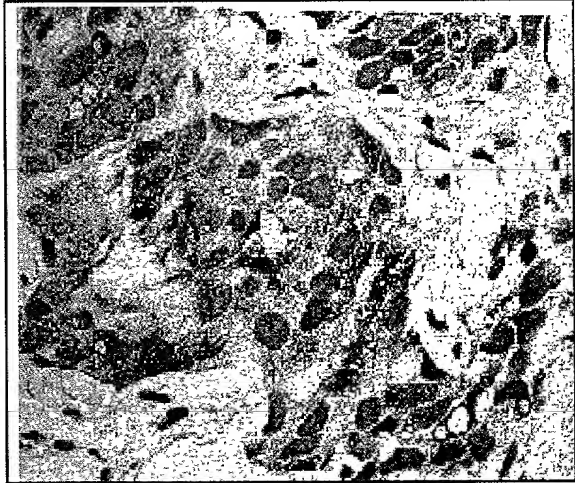Fig. 6: Immunohistochemical staining of PROST 03 expression: PROST 03 expressing cells are shown in red.
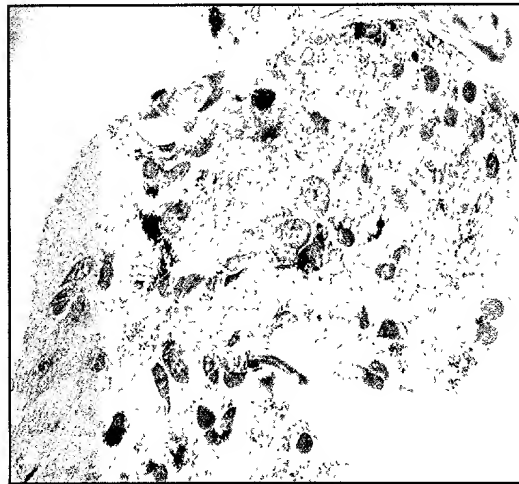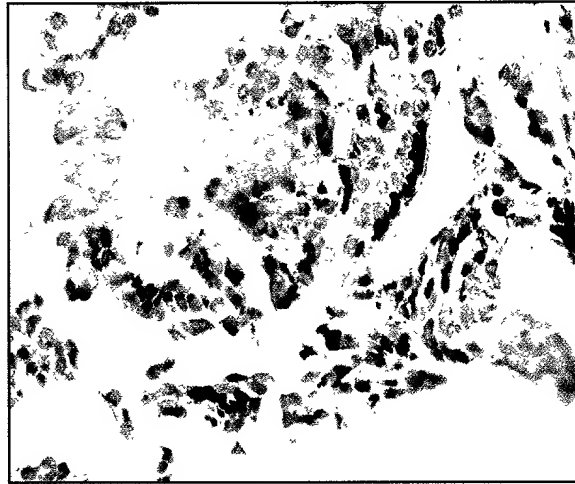

6a: Normal Prostate

6b: Prostate Carcinoma

6c: Lymph Node, Metastatic Prostate Carcinoma

6d: Bone Marrow, Metastatic Prostate Carcinoma

6e: Bone, Metastatic Prostate Carcinoma